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A; Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma		A;Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111 B:B=nnishhl7	A; Residues: 367-419 <mal3></mal3>	A; Molecule type: DNA A	A;ACCESSION: 1846UY	A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031	A; Molecule Type: INKNA A; Residues: 292-471, 'D', 473-810 <mal2></mal2>	A;Status: translated from GB/EMBL/DDBJ	A; Accession: 162738	A: Title: Characterization of a complementary deoxyribonucleic acid coding for human a a negeromore number - 145641. MITP 48707311	,	A:Experimental source: liver D:Walinowski D D: Gadior I F: Davie F W	A;Cross-references: GB:x05199; NID:g35530; PIDN:CAA28831.1; PID:g35531	A; MOJECULE CYPE: IIKNA A: Residues:] -47]. / V, 473-810 <for></for>	A;Accession: A26646	A; Reference number: A26646; MUID:87162490	A:Title: Molecular cloning and characterization of a full-length cDNA clone for human	R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.	A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613	A; Moldecule (ype: DNA A; Residues: 1-16 (AAAI)>	A;Status: translated from GB/EMBL/DDBJ	A; Accession: I52242	A; Reference number: 152242; MUID:91997523	Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990	R; Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;	A; Experimental source: leukocyte; lung fibroblast A; Experimental source: leukocyte; lung fibroblast	A; Residues: 1-810 (PET)	A; Molecule type: DNA	A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the f	R.Petersen, T.E.; Martzen, M.R.; IChinose, A.; Davie, E.W. T Biol Chem 265 6104-611 1990	C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625;	N;Contains: anglostatin; micropiasmin; plasminogen C;Species: Homo sapiens (man)	plasmin (EC 3.4.21.7) precursor [validated] - human N;Alternate names: plasminogen precursor [misnomer]	RESULT 1

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A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G. J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferation, R;Reference number: A58811; MUID:97067211
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                                                                                                                                                                                                                                                                   R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D. Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1
A;Reference number: A58812; MUID:9548733
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A;Title: Primary structure of the B-chain
A;Reference number: A04627; MUID:77225245
A;Accession: A04627
                                                                                    submitted to the Brookhaven Protein Data Bank, A; Reference number: A51488; PDB:2PK4
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A; Reference number: A51341; PDB:1PK4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: The primary structure of human plasminogen. II. A; Reference number: A92125; MUID: 73149248
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A; Residues: 20-71, 'E', 73-85,87-106, 'D', 108-360, 'E', 362-810
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Piol. Chem. 259, 13690-13694, 1984
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J. Biochem. 58, 539-547, 1975
                                          T.P.; Tulinsky, A
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Biochem. 50, 489-494,
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to the Brookhaven Protein Data ce number: A51911; PDB:1PKR
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                                                                                                                                                     376-454
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A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol
C;Superfamily: plasmin; kringle homology; duplication; fibrinolysis; glycoprotein; h
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; h
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 221, 927-937, 1994
A;Tit.le: (1)H-NNR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:119498; OMIM:173350 A; Map position: 6q26-6q27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Rejante, M.R.; Llinas, M.
Eur. J. Blochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex A;Reference number: A58817; MUID:94237158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Contents: annotation; conformation by R; Rejante, M.; Llinas, M. submitted to the Brookhaven Protein Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rejante, M.; Llinas, M. submitted to the Brookhaven Protein Data A;Reference number: A65803; PDB:1HPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, submitted to the Brookhaven Protein Data Bank, A;Reference number: A65980; PDB:1KRN
                                                                                                                                                                                                                                                           ns the walls
                                                                                                                                                                                                                                                                                                            A; Description:
                                                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                           A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: PLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ting solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rg-580,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Comment: Plasmin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents:
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A;Title: Crystal structure of the kringle 2 domain of tissue
A;Reference number: A39483; MUID:92118803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid
A;Reference number: A58818; MUID:92031503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the Brookhaven Protein Data Bank, A; Reference number: A65245; PDB:1CEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: annotation; conformation by (1)H-NMR, residues 103-18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A65804; PDB:1HPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents:
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A;Title: Crystal and molecular structure of human plasminogen
A;Reference number: A58819; MUID:92031502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents:
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    20-810/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resulting
                                                                                                                                                                                                                                                                                                                                                                                           17/1; 62/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microplasmin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation
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, 30, 10589–10594, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.; Mathews, I.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation; X-ray crystallography,
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                                                                                                                                                                                                                                                       n: dissolves the fibrin of blood clots; acts as a proteolytic of the graafian follicle; also activates the urokinase-type properties.
plasminogen #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) imme in two chains connected by two disulfide bonds. Without the lasmin is formed by autolytic cleavage of plasmin under artifly lysin 1 (see PIR:KCHUS1) acts on plasminogen to produce anglo
                                                                                                                                                                                                                                                                                                                                                                                       98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1)H-NMR, residues 103-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tulinsky, A.; Westbrook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kringle 4 refined
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ut the inhibit
r artificial c
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                                                                                                                                                                                                                                                           plasminogen
                                                                                                                                                                                                                                                                                                            factor
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F;1-9/Domain: signal sequence #status precursor nomology <PLPH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;481-560/Domain: kringle homology <KR5>
F;481-560/Domain: kringle homology <KR5>
F;481-560/Domain: kringle homology <KR5>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32-
Donds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmin (EC 3.4.21.7) precursor - rhesus macaque (;Species: Macaca mulatta (rhesus macaque) C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 C;Accession: B32869; B30848 R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M. J. Biol. Chem. 264, 5957-5965, 1989 A;Title: Rhesus monkey apollpoprotein(a). Sequence, A;Reference number: A32869; MUID:89174660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;79-466/Product: angiostatin #status experimental <AST>
F;97-580,581-810/Product: plasmin #status experimental <MATP
F;97-580/Comain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;103-181/Domain: kringle homology <KR2>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;377-456/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
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                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: plasmin; kringle homology; plasminogen-related protein precursor Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase; l-96/Domain: plasminogen-related protein precursor homology <PLPH>
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ross-references: GB:J04697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cule type: mRNA
idues: 1-810 <TOM>
                                                                                                                                                                                             s: #status predicted
,665,760/Active site: His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
    98
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                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                      1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNSQVRWEYCKIPSCDSSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
VYLSECKTGNGKNYRGTMSKTRTGITCQKWSSTSPHRPTFSPATHPSEGLEENYCRNPDN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPWCHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPQGPWCYTTDPEKRYDYCDILECEEECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                       93.6%;
93.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID: g342272; PIDN: AAA36901.1; PID: g342273
                                                                                                                                                                                          Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1535; D
Pred. No. 7.1e
0; Mismatches
                                                                                 Score 1442; DB 2;
Pred. No. 4.5e-98;
"""matches 9;
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                                                                                                                              Length 810;
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F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;561-783/Domain: kringle homology <KR5>
F;561-783/Domain: trypsin homology <KRY>
F;561-783/Domain: trypsin homology <TRY>
F;501-43,34-42,84-102,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,
                                                                                                                                                                                                                                                                                                                                                                                                  A; Pathway: fibrinolysis
C; Superfamily: plasmin; kringle homology; plasminogen-related protein
C; Superfamily: plasmin; kringle homology; plasminogen-related protein
C; Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; pl
F; 1-790/Product: plasminogen #status predicted <PRO>
F; 1-77/Domain: plasminogen-related protein precursor homology (fragmen
F; 1-77/Domain: plasminogen-related protein precursor homology (fragmen
F; 1-77/Domain: activation peptide #status predicted <ACH>
F; 18-560/Product: plasmin chain A #status predicted <ACH>
F; 18-162/Domain: kringle homology <KR1>
F; 18-162/Domain: kringle homology <KR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-57 < BRU>
R; Marti, T.; Schaller, J.; Rickli, E.E.
R; Marti, T. Schaller, J.; Prickli, E.E.
Bur. J. Biochem. 149, 279-285, 1985
A; Title: Determination of the complete amino-acid
A; Reference number: A25834; MUID:85203907
A; Accession: A25834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J. Bur. J. Biochem. 114, 465-470, 1981 A;Title: Comparison of the primary structure A;Reference number: S03735; MUID:81212097 A;Accession: S03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in ns the walls of the graafian follicle; also activates the urokinase-type plasminoger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues:
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 450-790 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-560 <SCH>
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Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence
A;Reference number: S03733
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C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; A25834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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        F; 602, 645, 740/Active
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                                          #status predicted
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site: His, Asp,
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Query Match Best Local Similarity

83.9%;

Score 1292; Pred. No. 4

4e-87;

DB 1;

Length 790;

Matches

Conservative

23;

Mismatches

Indels

0

Gaps

0,

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Plasmin (EC 3.4.21./) precent plasmin (EC 3.4.21./) plasminogen N; Alternate names: plasminogen C; Species: Bos primigenius taurus (cattle) C; Species: Bos primigenius taurus (cattle) C; Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #te C; Accession: $45046; A25835; I45961; S03736 R; Berglund, L.; Andersen, M.D.; Petersen, T.E. submitted to the EMBL Data Library, May 1994 A; Description: Cloning and characterizatin of the bov **Peference number; $45046
A;Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney
F;1-26/Domain: signal sequence #status predicted <SIG>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
F;27-812/Product: plasminogen #status experimental <APT>
F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583/Domain: plasmin chain A #status experimental <AACH>
                                                                                                                                                                                                                                                                                                                                               A; SSION: 145961
A; Us: translated from GB/EMBL/DDBJ
A; MOIEcule type: mRNA
A; Residues: 706-743, 'R', 745-812 <MAL>
A; Cross-references: GB: K02935; NID: 9163551; PIDN: AAA30714.1; PID: 9163552
A; Cross-references: GB: K02935; NID: 9163551; PIDN: AAA30714.1; PID: 9163552
A; Cross-references: GB: K02935; NID: 9163551; PIDN: AAA30714.1; PID: 9163552
A; Cross-references: GB: K02935; NID: 9163551; PIDN: AAA30714.1; PID: 9163552
A; Cross-references: GB: K02935; NID: 9163551; PIDN: AAA30714.1; PID: 9163552
A; Moiecule type: mRNA
A; Accession: S03735; MOID: 81212097
A; Accession: S03736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, Eur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with hum A;Reference number: A25835; MUID:85203906
A;Accession: A25835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH>
R;Mallowski, D.P.; Sadder, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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C; Function:
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A; Residues: 27-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-812 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erence number: I45961; MUID:85023311
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F;282-359/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR4>
F;485-564/Domain: kringle homology <KR5
F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342
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F;192-269/Domain:
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                                                                                                                                                         GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK 180
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                                                                                                                                                                                                                                                                            IYLLECKTGNGQTYRGTTAETKSGYTCQKWSATSPHYPKFSPEKFPLAGLEENYCRNPDN 164
 TNSEVRWEYCTIPSCESSPL
                                                                   GTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENYCRNPNGEKAPWCYT
                                                                                                                                      GYIPSKFPNKNLKMNYCRNPDGEPRPWCFTTDPQKRWEFCDIPRCTTPPPSSGPKYQCLK
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210; Conserv
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                                260
 364
                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                               Score 1291; DB 1;
Pred. No. 4.9e-87;
3; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <KR1>
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                                                                                                    240
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                                                                     344
                                                                                                                                      284
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RESULT 5

plasmin (EC 3.4.21.7) precursor - mucconstrains: angiostatin; plasminogen c; Species: Mus musculus (house mouse) c; Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999 c; Accession: A38514; \$48202; \$48203 R; Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W. Genomics 8, 49-61, 1990 A; Title: Characterization of the cDNA coding for mouse plasminogen and localization A; Reference number: A38514 AUID:91184812 A; Accession: A38514 A; MUID:91184812 A; Accession: A38514 A; MUID:91184812 A; Accession: A38514 A; MUID:91184812 A; Accession: A38514 A; Residues: 1-812 < DEG> A; Cross references: GB:J04766; NID:9200402; pIDN:AAA50168.1; PID:9200403 A; Cross references: GB:J04766; NID:9200402; pIDN:AAA50168.1; PID:9200403 A; Title: Characterization of the murine plasma fibrinolytic system. A; Reference number: S48202; MUID:95010076 A; Accession: S48202; MUID:95010076 A; Accession: S48203 A; Molecule type: protein A; Residues: 20-25 < LIJ> A; Molecule type: protein A; Residues: 22-27 < LI2>

C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmediately after dissociation from the clot. In the presence of the inhibitor, the act e inhibitor, the activation involves also removal of the activation peptide. C;Comment: Stromelysin 1 (see PIR:KCMSSI) acts on plasminogen to produce angiostatin. eful in treating solid tumors.

A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in ns the walls of the graafian follicle; also activates the urokinase-type plasminogen

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F:20-96/Domain: activation peptide #status predicted <APT>
F:79-466/Product: angiostatin #status predicted <AST>
F:79-581,582-812/Product: plasmin #status predicted <AKT>
F:97-581,582-812/Product: plasmin #status predicted <AKT>
F:97-581/Domain: chain A #status predicted <ACH>
F:103-181/Domain: kringle homology <KR2>
F:183-182/Domain: kringle homology <KR2>
F:275-352/Domain: kringle homology <KR2>
F:377-454/Domain: kringle homology <KR4>
F:377-454/Domain: kringle homology <KR4>
F:377-454/Domain: chain B #status predicted <BCH>
F:481-560/Domain: chain B #status predicted <BCH>
F:482-805/Domain: chain B #status predicted <BCH>
F:4973,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,
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C; Superfamily: plasmin; kringle homology; plasminogen-related protein
C; Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis;
C; Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis;
C; Keywords: angiogenesis inhibitor; blood; protein precursor homology <PLPH>
F; 1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 1-19/Domain: signal sequence #status predicted <PRO>
                                                    A;Cross-references: EMBL:U33171; NID:g1046360; PID:g1046361 C;Superfamily: plasmin; kringle homology; plasminogen-related C;Keywords: hydrolase; serine proteinase F;1-96/Domain: plasminogen-related protein precursor homology F;103-181/Domain: kringle homology <KR1>F;185-262/Domain: kringle homology <KR2>
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A;Molecule type: mRNA
A;Residues: 1-810 <LAW>
                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a):
A;Reference number: I46259; MUID:96025778
A;Accession: I46260
                                                                                                                                                                                                                                                                                                                                                                                                          R; Lawn, R.M.; Boonmark, J. Biol. Chem. 270, 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C;Accession: I46260
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9/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

19/Cleavage site: carbohydrate (Asn) (covalent) #status predicted

106-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

1581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

1524,667,762/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-812/Product: plasminogen #status predicted <PRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYLSECKTGIGNGYRGTMSRTKSGVACQKWGATFPHVPNYSPSTHPNEGLEENYCRNPDN 157
: kringle homology 
: kringle homology 
: kringle homology 
: kringle homology 
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                                                                                                                                                                                                                                                                                                                                                                                                                           Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne,
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Pred. No. 8.5e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Insights
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.5e-86;
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                                                                                                                                                                          homology
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R.Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, J. Biol. Chem. 270, 24004-24009, 1995
A.;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog a A; Reference number: 146259; MUID:96025778
A; Accession: T18518
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apolipoprotein(a) - western European hedgehog (fragment) C;Species: Erinaceus europaeus (western European hedgehog) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_c C;Accession: T18518
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T18518
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                                                                                                                                                                                                                                                                                     QΥ
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A; Residues: 1-2869 <LAW>
A; Cross-references: EMBL:U33170;
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                                                                                                                  DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: liver C; Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                           ent apolipoprotein(a).
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                                             GWRKQTPHRHEYTPENYPSKNLFGNYCRNPDGEIAPWCYTTNSAVRWEYCSIPTCESSSP
                                                                                                                                                                                                                                                                         LSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPPSSGPTYQCLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYLSECKVGNGKYYRGTVSKTKTGLTCQKWSAETPHKPRFSPDENPSEGLDQNYCRNPDN
RNPDGKRAPWCHTTNSQVRWEYCKIPSCDSS
                                                                                                                                                                                      VAPWCYTTNSAMRWEYCSIPACESPTPPTEHLVVPEQCLEGNGENYQGNMAITVSGQPCQ
                                                                                                                                                                                                                    QGPWCYTTDPEKRYDYCDILECE-----EECMHCSGENYDGKISKTMSGLECQ
                                                                                                                                                                                                                                                     VDQCLEGTGENYRGNMAVTASGHTCQRWREQSPHSHSRTPENYPTKNLVGNYCRNPDGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNSSVRWEFCKIPDCVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKGPWCYTMDPEVRYEYCEIIQCEDECMHCSGQNYVGKISRTMSGLECQPWDSQIPHPH
                                                                                                                                                   AWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCTTPPP
                                                                                                                                                                                                                                                                                                                        149;
                                                                                                                                                                                                                                                                                                                        Conservative
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55.0%;
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Pred.
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No. 1.5e-56;
                 258
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C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114;
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
   A; Experimental source: plasma R; Weidner, K.M.; Behrens, J.; J. Cell Biol. 111, 2097-2108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846
R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte grow A;Reference number: A33512; MUID:89392017
A; Ssion: A33512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936 R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, Biochem. Biophys. Res. Commun. 172, 321-327, 1990 A;Title: Isolation and expression of cDNA for different forms of hepatocyte A;Reference number: A36677; MUID:91025062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H. Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
A;Note: the JIPID, March 1991
S;Description: Organization of the human hepatocyte growth factor-encoding
A;Perence number: JU0333
A;Perence number: JU0333
A;Cule type: DNA
A;Cule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: JH0579; MUID:91340155
A;Accession: JH0579
                                                                                           A; Molecule type: protein A; Residues: 32-43;53-58 < YOS>
                                                                                                                                                                                                                A:Experimental source: embryonic lung R;YoShiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy
                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-161,167-728 <RUB>
A;Cross-references: GB:M55379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-161,167-728 <SE4>
A; Cross-references: EMBL: X16323
                                                                                                                                                              A; Accession:
                                                                                                                                                                                          A; Reference number: PH0114; MUID: 91207365
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A; Residues: 1-728 <SE3>
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A; Residues: 1-728 <SEK>
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A;Residues: 1-728 <WEI>
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A;Accession: A36677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a39006; MUID:91110540
         Vandekerckhove,
1990
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                                  Birchmeier,
                                                                                                                                                                                                                heavy chain
                                                                                                                                                                                                                                                                            S.; Kondo,
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                                                                                                                                                                                                                   of
                                                                                                                                                                                                                   both
                                                                                                                                                                                                                                                                                J.; Nakayama,
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                                                                                                                                                                                                                   native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A37796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatoc
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A; Map position: 7q21.1-7q21.1
A; Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; C; Complex: disulfide-bonded heterodimer of chains derived C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: alternative splicing; glycoprotein; growth F;1-31/Domain: signal sequence #status predicted <SIG> F;32-494,495-728/Product: hepatocyte growth factor #str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; R;Shina, N.; Naggo, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Hi Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from A;Reference number: 152253; MUID:92062058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: the authors translated the codon CAG for residue 727 as Glu A;Note: part of this sequence, including the amino end of both the alpha and beta ch R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Bi Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth A;Reference number: I59214; MUID:93087571
                                                                                                                                                                F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status experi F;294,402,566,653/Binding site: carbohydrate (Asn) (covalent) *status predicted F;487-604/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                              F;305-383/Domain: kringle homology <KR3>F;301-469/Domain: kringle homology <KR4>F;495-728/Domain: beta chain #status experimental <BCH>F;495-716/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N. Eur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from A;Reference number: $15443; MUID:91200041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-288, 'EB' <HAR>
A; Residues: 1-288, 'EB' <HAR>
A; Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
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A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-38
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
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A; Nolecule type: B6-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'A; R; Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Nature 342, 440-443, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                        F;128-206/Domain: kringle homology <KR1>F;211-288/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 161-166 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-288, 'ET' <MIY2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: I59214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Molecular cloning and expression of human hepatocyte growth factor A; Reference number: S06794; MUID:90066676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Scatter factor: molecular characteristics and effect on A; Reference number: A37796; MUID:91035621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;32-494/Domain: alpha chain #status experimental <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:127524; OMIM:142409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: HGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
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                             Query Match
Best Local
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                             51.8%;
                             Score 797;
Pred. No. 5.
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-51;
81;
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Higashio, K.
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Matches

2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND 61

Mismatches

Indels

6;

Gaps

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A; Molecule type: mRNA
A; Residues: 1-728 < ORA>
A; Residues: 1-728 < ORA>
A; Residues: 1-728 < ORA>
Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C; Taplex: disulfide-bonded heterodimer of chains derived from the same precursor cription: stimulates mitosis of hepatocytes and other cells
A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology: trypsin homology
C; Superfamily: hepatocyte growth factor; kringle homology: trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F; 1-32/Domain: signal sequence #status predicted <SIO>
F; 1-32/Domain: signal sequence #status predicted <MAT>
F; 56-495/Product: hepatocyte growth factor #status predicted <ACH>
F; 121-289/Domain: kringle homology <KR1>
F; 212-289/Domain: kringle homology <KR1>
F; 396-728/Domain: kringle homology <KR2>
F; 496-728/Domain: kringle homology <KR4>
F; 496-728/Domain: krypsin homology <KR4>
F; 496-728/Domain: trypsin homology <KR4>
F; 496-728/Domain: krypsin homology <KR4+
F; 496-728/Domain: krypsin homology <KR4+
F; 496-728/Domain: krypsin homology <KR4+
F; 
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A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of the A;Reference number: A35644; MUID:90222197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A35644; A; Accession: A35644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-728 <TAS>
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C;Accession: A35644; S13211
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N;Alternate names: hepapoietin A; scatter factor
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                Query Match
Best Local S
Matches 132
                                                                                                                                                                                                                                               33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status 295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted 488-607/Disulfide bonds: #status predicted
        125
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                                                                                                                                          Similarity
                                                                                                                   Conservative
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49.
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Pred.
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                                                                                                                Mismatches
                                                                                                                                       782; DB 1;
No. 6.9e-50;
                                                                                                                84;
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                                                                                                                                                              Length 728
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                                                                                                             Gaps
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A; Residues: 1-710 < NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: I51283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Nakamura, H.;
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                               291
                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND
                            KGQGEGYRGSVSTTYNGIQCQRWDSQFPHLHNFTPENYKCKDLSENYCRNPDGSESPWCF
                                                                                KGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCH
                                                                                                                                                                                        GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCT-TPPPSSGPTYQCL 179
                                                                                                                                                                                                                                                                                                      POGPWCYTTDPEKRYDYCDILECEE-ECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH
                                                                                                                                                                                                                                                                                                                                                            YIRDCIHGKGSNYRGTRNVTKRGLACQPWNSMIPHEHSFLPSTYRGKDLKENYCRNPKGE
                                                                                                                                                                                                                                                     EGGPWCFTKSPEVRHDVCDIPFCSEVDCVTCNGEHYRGPMDYTESGKECQRWDLQRPHKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130;
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39;

Pred. No. Mismatches

1.7e-49;

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Indels

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Gaps

w ••

120 170 61

230

239

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A;Cross-reterences: GB:S77422; NID:g998932; PIDN:AAB34354.1; PID:g998933
A;Cross-reterences: GB:S77422; NID:g998932; PIDN:AB34354.1; PID:g998933
A;Cross-reterences: GB:S77422; PIDN:G9984354; NID:g998932; PIDN:AB34354.1; PID:g998933
A;Cross-reterences: GB:S77422; PIDN:G9984354; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999 C;Accession: I51283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatocyte growth factor precursor - clawed frog N;Alternate names: hepapoietin A; scatter factor C;Species: Xenopus sp. (clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Molecular cloning of Xenopus HGF cDNA and A; Reference number: I51283; MUID:95267690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APWCHTTNSQVRWEYC-KIPSCDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFLPERYPDKGFDDNYCRNPDGKPRPWCYTLDPDTPWEYCAIKMCAHSAVNETDVPME--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tashiro, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1995
50.4%;
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                                                    Score 776.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clawed frog
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                                                                                                                                                                                                                                                         carbohydrate (Asn) (covalent) #status
                                              DB 1;
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                                              Length 710;
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A;Molecule type: protein
A;Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
A;Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
A;Residues: 496-607,'X',509-512,'L',514-516,'X',518-519 <NAT>
A;Residues: 496-607,'X',518-519 <A;Particular Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Reference number: 148758; MUID:95122532
A;Accession: 148758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Llu, Y.; Michalopoulos, G.K.; Zarnegar, R. Biochim. Biophys. Acta 1216, 299-303, 1993
A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growtl A;Reference number: S43416; MUID:94060105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoletin A; scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
C;Accession: JC2117; PC2004; A60185; S43416; S45521; S17173; S10966; I48758;
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Blochem. Biophys. Res. Commun. 199, 772-779, 1994
                               A; Molecule type: DNA
A; Residues: 1-30 < RES>
                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Hepatocytes and scatter factor. A; Reference number: S10966; MUID:90326152
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A;Title: Purified scatter factor stimulates epithelial and vascular endothelial A;Reference number: A60185; MUID:90377927
A;Accession: A60185
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      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A: Reference number: S45521
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A; Residues: 1-728 <SAS2>
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A; Accession: JC2117
                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S10966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 496-517, 'T', 519 <COF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S17173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: protein
;Molecule type: protein
;Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,'E'
;Llu, Y.; Michalopoulos, G.K.; Zarnegar, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-728 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein Residues: 496-504 <SA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:D10212; NID:g220435; PIDN:BAA01064.1; PID:g220436; PIDR:grimental source: fibroblast, COS-1 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Residues: 1-563,'H',565-728 <LI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
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Title: Purification and characterization
Reference number: S17173; MUID:91354223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oss-references: EMBL:X72307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. 278, 35-41, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTDPNIRIGHCSQIKKCQAS
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   EMBL: X81630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library, May 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1993
NID:g673451; PIDN:CAA57286.1; PID:g673452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biologically active scatter factor
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                         F;72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <AAT>
F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <AC
F;110-186/Domain: kringle homology <KRII>
F;191-268/Domain: kringle homology <KRII2>
F;292-370/Domain: kringle homology <KRI3>
F;292-370/Domain: kringle homology <KRI3>
F;39-457/Domain: kringle homology <KRI4>
F;489-716/Domain: kringle homology <KRI4
F;489-709/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-716 <OHS>
A; Cross-references: EMBL: x95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719
A; Cross-references: EMBL: x95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719
C; Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: duplication; glycoprotein; growth factor; kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kr
F; 1-32/Domain: signal sequence #status predicted <SIG>
F; 56-495/Domain: signal sequence #status predicted <MAT>
F; 56-495/Domain: hepatocyte growth factor #status predicted <ACH>
F; 129-207/Domain: kringle homology <KR1>
F; 129-207/Domain: kringle homology <KR2>
F; 3106-384/Domain: kringle homology <KR3>
F; 3106-384/Domain: kringle homology <KR3>
F; 307-38/Domain: kringle homology <KR3>
F; 307-38/Domain: kringle homology <KR4>
F; 496-719/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F; 496-719/Domain: trypsin homology <KR4>
F; 496-719/Domain: trypsin homol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Molecular cloning of rat macrophage-stimulating protein and A; Reference number: {\tt JC5061}; MUID: 97011126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macrophage-stimulating protein 1 precursor -
C;Species: Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ohshiro, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: JC5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 TYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 KFLPERYPDKGFDDNYCRNPDGKPRPWCYTLDPDTPWEYCAIKTCAHSAVNETDVPME--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 APWCHTTNSQVRWEYC-KIPSCDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 YIRNCIIGKGGSYKGTVSITKSGIKCQPWNSMIPHEHSFLPSSYRGKDLQENYCRNPRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PQGPWCYTTDPEKRYDYCDILECEE-ECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPWCFTTDPNIRVGYCSQIPKCDVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto,
rs. Res. Commun. 227, 273-280, 1996
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Pred. No. 1.9e-49;
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A;Cross-references: GB:S77480; NID:g998675; PID:g998676 C;Superfamily: hepatocyte growth factor; kringle homolog F:124-197,Domain: kringle homology <KRG>F:202-279,Domain: kringle homology <KR2>F:296-374/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its express A;Reference number: I51285; MUID:95237013
A;Accession: I51285
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-411 <STR>
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RESULT
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Best Local S
Matches 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 RNKVKASNCFRGKGEDYRGTTNTTSAGVPCQRWDAQNPHQHRFVPEKYACKDLRENFCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 132; Conserver
                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
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                                                                                                                                                                                                                                                                                    PQGPWCYTTDPEKRYDYCDILECEE-ECMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                       YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFHPEKFPDKALKDNYCRNPDASERPWCYTTDPNVEREFCDLPSCGPNLPPTTKGSKSQQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRC--TTPPPSSGPTYQ- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRGPWCYTTNRSVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDLQHPHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVRTCIMDNGASYRGTVARTADGLPCQAWSRRFPNDHKYTPT--PKNGLEENFCRNPDGD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND
                                                                                    WCHTTNSQVRWEYC-KIPSCDSS 258
                                                                                                                       TCIQGQGEGYRGTVNTIWSGIQCQRWDSQFPHQHNITPENFKCKDLRENYCRNPDGSESP
                                                                                                                                                         QCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAP 236
                                                                                                                                                                                                                                                                                                                                    YVRNCIIGKGAEYKGTISITKSGIQCQAWNSMIPHE-----HSYRGKDLRENYCRNPRGE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGKRAPWCHTTNSQVRWEYC-KIPSCDSSPV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQGPWCYTTDPEKRYDYCDILECEEE-CMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                  WCFTTDPNIRIGYCSQIPKCDVS
                                                                                                                                                                                          KFRPERYPDKGFDDNYCRNPDGKLRPWCYTLDPNTPWEFCAIKTCDVGILNSTEAVAETT
                                                                                                                                                                                                                                                                 EGGPWCFTTSPQMRHEVCDIPLCSEVECMTCNGESYRGPMDHTESGKECQRWDLQRPHKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDGSEAPWCFTSRPGLRVAFCYQIPRCTEEVV 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRN
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50.2%;
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Pred. No. 9.2e-49;
36; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 754.5;
Pred. No. 4e-4
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
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                                                                                                                                                                                                                                                                                                                                                                                                                            4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology;
                                                                                                                                                                                                                                                                                                                                                                                                           ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                               411;
                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gherard
                                                           apoprotein(a) (EC 3.4.21.-) precursor [validated] - human N;Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a) C;Species: Homo sapiens (man) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000 C;Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286 R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless Mature 330, 132-137, 1987
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A; Residues: 1-716 <D
           A; Reference number: A; Accession: S00657
                                              A;Title: cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: B40332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                             nce of human apolipoprotein(a) is $00657; MUID:88039109
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C;Complex: disulfide-bonded heterodimer of chains derived from the same precurso:
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIG>
F;19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <F:19-488/Domain: alpha chain #status experimental <ACH>
F;19-489/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;292-370/Domain: kringle homology <KR3>
F;399-457/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #status experimental <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;489-709/Domain: trypsin homology <TRY>
F;489-709/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: hepatocyte growth factor-like protein C;Specles: Mus musculus (house mouse) C;Pecles: Mus musculus (house mouse) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999 C;Accession: A40332; B40332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M74181; NID:g193833; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, Biochemistry 30, 9781-9791, 1991
A;Title: Characterization of the mouse cDNA and A;Reference number: A40332; MUID:92002017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-18,'P',20-716 <DEG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 18/1; 67/2; 105/1; 143/2; 189/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:M74180; NID:g193831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                macrophage-stimulating protein 1 precursor -
                                 Local Similarity
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <DEG>
                                 48.98;
                                 Score 753.5; DB 1
Pred. No. 8.2e-48;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229/2; 269/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN: AAA50166.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAA50167.1; PID: g193834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene coding
      86;
      Indels
                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the same precursor trypsin homology
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      15;
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Gaps
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2 YLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDND 61
                                                                                                                                                                                                                                                   PFQPEKFLDKDLKDNYCRNPDGSERPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQR
                                                        PDGKRAPWCHTTNSQVRWEYC-KIPSC
                                                                                                                        RNKGKALNCFRGKGEDYRGTTNTTSAGVPCQRWDAQSPHQHRFVPEKYACKDLRENFCRN
                                                                                                                                                         -SSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRN 229
                                                                                                                                                                                                                                                                                                            GYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRC--TTPPP-----
                                                                                                                                                                                                                                                                                                                                                                                  PRGPWCYTTNRSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                              PQGPWCYTTDPEKRYDYCDILECEEE-CMHCSGENYDGKISKTMSGLECQAWDSQSPHAH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVRTCIMDNGVSYRGTVARTAGGLPCQAWSRRFPNDHKYTPT--PKNGLEENFCRNPDGD 163
PDGSEAPWCFTSRPGLRMAFCHQIPRC
                                                               255
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                                                                                                                                                                                                                                                                                                                   170
                                                                                                                                                                                                                                                                                                                                                                                  223
                                                                                                                              343
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homologous

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plasminogen

Chen, E.Y.; Fless, G.M.;

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F;142-219/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;370-447/Domain: kringle homology <KR4>
F;484-561/Domain: kringle homology <KR5>
F;598-675/Domain: kringle homology <KR5>
F;598-675/Domain: kringle homology <KR6>
F;712-789/Domain: kringle homology <KR7>
F;826-903/Domain: kringle homology <KR8>
F;940-1017/Domain: kringle homology <KR8>
F;940-1017/Domain: kringle homology <KR9>
F;1054-1131/Domain: kringle homology <KR10>
F;1168-1245/Domain: kringle homology <KR11>
F;1282-1359/Domain: kringle homology <KR12>
F;1396-1473/Domain: kringle homology <KR13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rs of kringle repeats
C;Superfamily: apolipoprotein(a); kringle homology; trypsin
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein;
F;1-19/Domain: signal sequence #status predicted <SIG>
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R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Saccc Pro Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A; e: Characterization by yeast sticical chromosome cloning of the linked apolipopr A; erence number: A47233; MUID:93087573
A;Accession: I60906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X',4396-4401 <EAT>
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A;Title: 5' control regions of the apolipoprotein(a) gene and members of the A;Reference number: A47277; MUID:93165698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;20-4548/Product: apolipoprotein(a) #status
F;28-105/Domain: kringle homology <KR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-16 < RE4 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated A; Reference number: I52415; MUID: 92207924
A; Accession: I52415
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A; Accession: A28017
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A;Cross-references: 6B:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620 R;Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M86877; NID:g178780; PIDN:AAB49909.1; PID:g553185
A;Note: apo(a) gene 1 (nomenclature of reference I52415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-16 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-16 < RE5>
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A; Accession: A47233
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A; Residues: 1-16 <RES>
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A; Residues: 20-21,'p',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Ichinose, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-16 <RE2>
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pposition: 6q26-6q27
pte: several genes closely linked on chromosome 6 are identical in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s-references: GB:M86878; NID:g178782; PIDN:AAA51749.1;
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                                                                                                                                                                                                                                                       3779 VQDCYHGDGQSYRGSFSTTVTGRTCQSWSSMTPHWHQRTTEYYPNGGLTRNYCRNPDAEI 3838
                                                                                                                                                     3898 RGDGQSYRGTLSTTITGRTCQSWSSMTPHWHRRIPLYYPNAGLTRNYCRNPDAEIRPWCY 3957
                                                                                                                           150
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                       246 RWEYCKIPSCDSS
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                                                                                                                                                                                                                               63 QGPWCYTTDPEKRYDYCDILECE-----
                                                                                                                                                                                                                                                                               3 LSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDP 62
                                                 YRGISSTTYTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPWCYTTDPCV
                                                              YRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENYCRNPDGKRAPWCHTTNSQV 245
                                                                                                                                                                             HCSGENYDGKISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCF 149
                                                                                                                                                                                                                                                                                                          129;
RWEYCNLTQCSET
                                                                                                  IMDPSVRWEYCNLTRCPVTESSYLTTPTVAPVPSTEAPSEQAPPEKSPVVQDCYHGDGRS 4017
                                                                                                                          TTDPNKRWELCDIPRC----TTP-----
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